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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/784,528

DATE: 08/30/2004

TIME: 14:56:52

Input Set : N:\CrF3\RULE60\10784528.raw.txt

Output Set: N:\CRF4\08302004\J784528.raw

1 <110> APPLICANT: Case Western Reserve University
 2 Brown, Arthur M.
 3 Wible, Barbara A.
 4 <120> TITLE OF INVENTION: Methods of Inducing Apoptosis in Hyperproliferative Cells
 5 <130> FILE REFERENCE: 22884/04047
 6 <140> CURRENT APPLICATION NUMBER: US/10/784,528
 7 <141> CURRENT FILING DATE: 2004-02-23
 8 <150> PRIOR APPLICATION NUMBER: US/10/000,778
 9 <151> PRIOR FILING DATE: 2001-10-31
 10 <160> NUMBER OF SEQ ID NOS: 2
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1725
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 17 <400> SEQUENCE: 1

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20	cccatccccca aacgcgtt ggccccctggc accctgctgg gccccaaagcg tgagggtggac	180
21	atgcacccccc ctctgccccca gcctgtgcac cctgtatgtca ccatgaaacc attgcccttc	240
22	tatgaagtct atggggagct catccggccc accacccttgc catccacttc tagcagcgg	300
23	tttggagaag cgcaacttac ctttgcctc acaccccgac aagtgcagca gattttaca	360
24	tccagagagg ttctgccagg agccaaatgt gattatacca tacaggtgca gctaagggttc	420
25	tgtctctgtg agaccagctg ccccccaggaa gattattttc cccccaacct ctttgtcaag	480
26	gttaatggga aactgtgccc cctgcccgggt taccttccccca aaccaagaa tggggccgag	540
27	cccaagggc ccagccgccc catcaacatc acacccctgg ctcgactctc agccactgtt	600
28	cccaacacca ttgtggtaa ttggcatct gagttcgac ggaattactc cttgtctgtg	660
29	tacctggta ggcagtgtac tgcaggaacc cttctacaaa aactcagagc aaagggtatc	720
30	cggAACCCAG accactcgcg ggcactgatc aaggagaaat tgactgtga ccctgacagt	780
31	gaggtggcca ctacaagtct cccgggtgtca ctcatgtgcc cgctaggaa gatgcgcctg	840
32	actgtccctt gtcgtccct cacctgtgcc cacctgcaga gttcgatgc tgcccttat	900
33	ctacagatga atgagaagaa gcctacatgg acatgtcctg tgtgtgacaa gaaggtccc	960
34	tatgaatctc ttatcattga tggtttattt atggagattc ttatgttctg ttcaattgt	1020
35	gatgagatcc aattcatggaa agatggatcc tgggtggccaa tggaaacccaa gaaggaggca	1080
36	tctgaggttt gccccccgccc agggtatggg ctggatggcc tccagttacag cccagtcac	1140
37	ggggggagatc catcagagaa taagaagaag gtcgaagtttta ttgactgtac aatagaaagc	1200
38	tcatcagatg aggaggatct gccccctacc aagaagact gttctgtcac ctcagctgcc	1260
39	atccggccc tacctggaaag caaaggatgc ctgacatctg gccaccagcc atccctgggt	1320
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43	gcccttggcc acttcttcca gtaccgaggg accccctctc actttctggg cccactggcc	1560
44	cccacgctgg ggagctccca ctgcagcgcc actccggcgc cccctctgg ccgtgtcagc	1620

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45      agcattgtgg cccctgggg ggccttgagg gaggggcatg gaggaccct gccctcaggt    1680
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49 <211> LENGTH: 574
50 <212> TYPE: PRT
51 <213> ORGANISM: Homo sapiens
52 <400> SEQUENCE: 2
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56      20          25          30
57      Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala
58      35          40          45
59      Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro
60      50          55          60
61      Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe
62      65          70          75          80
63      Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr
64      85          90          95
65      Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro
66      100         105         110
67      Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala
68      115         120         125
69      Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu
70      130         135         140
71      Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys
72      145         150         155          160
73      Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys
74      165         170         175
75      Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro
76      180         185         190
77      Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp
78      195         200         205
79      Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg
80      210         215         220
81      Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile
82      225         230         235          240
83      Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala
84      245         250         255
85      Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met
86      260         265         270
87      Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr
88      275         280         285
89      Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn
90      290         295         300
91      Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro
92      305         310         315          320
93      Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser
94      325         330         335

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95 Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys
96 340 345 350
97 Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly
98 355 360 365
99 Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro
100 370 375 380
101 Ser Glu Asn Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser
102 385 390 395 400
103 Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val
104 405 410 415
105 Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr
106 420 425 430
107 Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr
108 435 440 445
109 Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro
110 450 455 460
111 Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe
112 465 470 475 480
113 Leu Gln Thr Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu
114 485 490 495
115 Asp Glu Gln Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro
116 500 505 510
117 Ser His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys
118 515 520 525
119 Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala
120 530 535 540
121 Pro Gly Gly Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly
122 545 550 555 560
123 Pro Ser Leu Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp
124 565 570

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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

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